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RAW SEQUENCE LISTING

DATE: 02/07/2002

PATENT APPLICATION: US/10/055,061

TIME: 11:09:48

Input Set : N:\Cr3\RULE60\10055061.raw

Output Set: N:\CRF3\02072002\J055061.raw

1 <110> APPLICANT: Bertin, John
 2 <120> TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
 3 PROTEIN FAMILY AND USES THEREOF
 4 <130> FILE REFERENCE: 07334-076001
 5 <140> CURRENT APPLICATION NUMBER: 10/055,061
 6 <141> CURRENT FILING DATE: 2002-01-22
 8 <150> PRIOR APPLICATION NUMBER: US/09/099,041A
 9 <151> PRIOR FILING DATE: 1998-06-17
 12 <150> PRIOR APPLICATION NUMBER: 09/019,942
 13 <151> PRIOR FILING DATE: 1998-02-06
 14 <160> NUMBER OF SEQ ID NOS: 37
 15 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 1931
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Homo sapiens
 21 <220> FEATURE:
 22 <221> NAME/KEY: CDS
 23 <222> LOCATION: (214)...(1833)
 24 <400> SEQUENCE: 1

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26	tgggcgcct cgtgacctag tgttcggggg caaaaagggg cttgccggcc tcgtcgtgc	120
27	aggggcgtat ctgggcgcct gacgcggcg tgggagcctt gggagccgcc gcagcagggg	180
28	gcacaccgg aaccggcctg agcggccggg acc atg aac ggg gag gcc atc tgc	234
29	Met Asn Gly Glu Ala Ile Cys	
30	1 5	
31	agc gcc ctg ccc acc att ccc tac cac aaa ctc gcc gac ctg cgc tac	282
32	Ser Ala Leu Pro Thr Ile Pro Tyr His Lys Leu Ala Asp Leu Arg Tyr	
33	10 15 20	
34	ctg agc cgc ggc gcc tct ggc act gtg tcg tcc gcc cgc cac gca gac	330
35	Leu Ser Arg Gly Ala Ser Gly Thr Val Ser Ser Ala Arg His Ala Asp	
36	25 30 35	
37	tgg cgc gtc cag gtg gcc gtg aag cac ctg cac atc cac act ccg ctg	378
38	Trp Arg Val Gln Val Ala Val Lys His Leu His Ile His Thr Pro Leu	
39	40 45 50 55	
40	ctc gac agt gaa aga aag gat gtc tta aga gct gaa att tta cac	426
41	Leu Asp Ser Glu Arg Lys Asp Val Leu Arg Glu Ala Glu Ile Leu His	
42	60 65 70	
43	aaa gct aga ttt agt tac att ctt cca att ttg gga att tgc aat gag	474
44	Lys Ala Arg Phe Ser Tyr Ile Leu Pro Ile Leu Gly Ile Cys Asn Glu	
45	75 80 85	
46	cct gaa ttt ttg gga ata gtt act gaa tac atg cca aat gga tca tta	522
47	Pro Glu Phe Leu Gly Ile Val Thr Glu Tyr Met Pro Asn Gly Ser Leu	

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97  act tca agg tcc ctg cca gct cct caa gac aat gat ttt tta tct aga      1338
98  Thr Ser Arg Ser Leu Pro Ala Pro Gln Asp Asn Asp Phe Leu Ser Arg
99  360          365          370          375
100 aaa gct caa gac tgt tat ttt atg aag ctg cat cac tgt cct gga aat      1386
101 Lys Ala Gln Asp Cys Tyr Phe Met Lys Leu His His Cys Pro Gly Asn
102          380          385          390
103 cac agt tgg gat agc acc att tct gga tct caa agg gct gca ttc tgt      1434
104 His Ser Trp Asp Ser Thr Ile Ser Gly Ser Gln Arg Ala Ala Phe Cys
105          395          400          405
106 gat cac aag acc att cca tgc tct tca gca ata ata aat cca ctc tca      1482
107 Asp His Lys Thr Ile Pro Cys Ser Ser Ala Ile Ile Asn Pro Leu Ser
108          410          415          420
109 act gca gga aac tca gaa cgt ctg cag cct ggt ata gcc cag cag tgg      1530
110 Thr Ala Gly Asn Ser Glu Arg Leu Gln Pro Gly Ile Ala Gln Gln Trp
111          425          430          435
112 atc cag agc aaa agg gaa gac att gtg aac caa atg aca gaa gcc tgc      1578
113 Ile Gln Ser Lys Arg Glu Asp Ile Val Asn Gln Met Thr Glu Ala Cys
114          440          445          450          455
115 ctt aac cag tcg cta gat gcc ctt ctg tcc agg gac ttg atc atg aaa      1626
116 Leu Asn Gln Ser Leu Asp Ala Leu Leu Ser Arg Asp Leu Ile Met Lys
117          460          465          470
118 gag gac tat gaa ctt gtt agt acc aag cct aca agg acc tca aaa gtc      1674
119 Glu Asp Tyr Glu Leu Val Ser Thr Lys Pro Thr Arg Thr Ser Lys Val
120          475          480          485
121 aga caa tta cta gac act act gac atc caa gga gaa gaa ttt gcc aaa      1722
122 Arg Gln Leu Leu Asp Thr Thr Asp Ile Gln Gly Glu Glu Phe Ala Lys
123          490          495          500
124 gtt ata gta caa aaa ttg aaa gat aac aaa caa atg ggt ctt cag cct      1770
125 Val Ile Val Gln Lys Leu Lys Asp Asn Lys Gln Met Gly Leu Gln Pro
126          505          510          515
127 tac ccg gaa ata ctt gtg gtt tct aga tca cca tct tta aat tta ctt      1818
128 Tyr Pro Glu Ile Leu Val Val Ser Arg Ser Pro Ser Leu Asn Leu Leu
129          520          525          530          535
130 caa aat aaa agc atg taagtgactg tttttcaaga agaaatgtgt ttcataaaag      1873
131 Gln Asn Lys Ser Met
132          540
133 gatattttata aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      1931
135 <210> SEQ ID NO: 2
136 <211> LENGTH: 540
137 <212> TYPE: PRT
138 <213> ORGANISM: Homo sapiens
139 <400> SEQUENCE: 2
140 Met Asn Gly Glu Ala Ile Cys Ser Ala Leu Pro Thr Ile Pro Tyr His
141 1          5          10          15
142 Lys Leu Ala Asp Leu Arg Tyr Leu Ser Arg Gly Ala Ser Gly Thr Val
143          20          25          30
144 Ser Ser Ala Arg His Ala Asp Trp Arg Val Gln Val Ala Val Lys His
145          35          40          45
146 Leu His Ile His Thr Pro Leu Leu Asp Ser Glu Arg Lys Asp Val Leu

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147	50	55	60
148	Arg Glu Ala Glu Ile Leu His Lys Ala Arg Phe Ser Tyr Ile Leu Pro		
149	65	70	75
150	Ile Leu Gly Ile Cys Asn Glu Pro Glu Phe Leu Gly Ile Val Thr Glu		80
151		85	90
152	Tyr Met Pro Asn Gly Ser Leu Asn Glu Leu Leu His Arg Lys Thr Glu		95
153		100	105
154	Tyr Pro Asp Val Ala Trp Pro Leu Arg Phe Arg Ile Leu His Glu Ile		110
155		115	120
156	Ala Leu Gly Val Asn Tyr Leu His Asn Met Thr Pro Pro Leu Leu His		125
157		130	135
158	His Asp Leu Lys Thr Gln Asn Ile Leu Leu Asp Asn Glu Phe His Val		140
159	145	150	155
160	Lys Ile Ala Asp Phe Gly Leu Ser Lys Trp Arg Met Met Ser Leu Ser		160
161		165	170
162	Gln Ser Arg Ser Ser Lys Ser Ala Pro Glu Gly Gly Thr Ile Ile Tyr		175
163		180	185
164	Met Pro Pro Glu Asn Tyr Glu Pro Gly Gln Lys Ser Arg Ala Ser Ile		190
165		195	200
166	Lys His Asp Ile Tyr Ser Tyr Ala Val Ile Thr Trp Glu Val Leu Ser		205
167		210	215
168	Arg Lys Gln Pro Phe Glu Asp Val Thr Asn Pro Leu Gln Ile Met Tyr		220
169	225	230	235
170	Ser Val Ser Gln Gly His Arg Pro Val Ile Asn Glu Glu Ser Leu Pro		240
171		245	250
172	Tyr Asp Ile Pro His Arg Ala Arg Met Ile Ser Leu Ile Glu Ser Gly		255
173		260	265
174	Trp Ala Gln Asn Pro Asp Glu Arg Pro Ser Phe Leu Lys Cys Leu Ile		270
175		275	280
176	Glu Leu Glu Pro Val Leu Arg Thr Phe Glu Glu Ile Thr Phe Leu Glu		285
177		290	295
178	Ala Val Ile Gln Leu Lys Lys Thr Lys Leu Gln Ser Val Ser Ser Ala		300
179	305	310	315
180	Ile His Leu Cys Asp Lys Lys Lys Met Glu Leu Ser Leu Asn Ile Pro		320
181		325	330
182	Val Asn His Gly Pro Gln Glu Glu Ser Cys Gly Ser Ser Gln Leu His		335
183		340	345
184	Glu Asn Ser Gly Ser Pro Glu Thr Ser Arg Ser Leu Pro Ala Pro Gln		350
185		355	360
186	Asp Asn Asp Phe Leu Ser Arg Lys Ala Gln Asp Cys Tyr Phe Met Lys		365
187		370	375
188	Leu His His Cys Pro Gly Asn His Ser Trp Asp Ser Thr Ile Ser Gly		380
189	385	390	395
190	Ser Gln Arg Ala Ala Phe Cys Asp His Lys Thr Ile Pro Cys Ser Ser		400
191		405	410
192	Ala Ile Ile Asn Pro Leu Ser Thr Ala Gly Asn Ser Glu Arg Leu Gln		415
193		420	425
194	Pro Gly Ile Ala Gln Gln Trp Ile Gln Ser Lys Arg Glu Asp Ile Val		430
195		435	440
			445

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196      Asn Gln Met Thr Glu Ala Cys Leu Asn Gln Ser Leu Asp Ala Leu Leu
197          450                      455                      460
198      Ser Arg Asp Leu Ile Met Lys Glu Asp Tyr Glu Leu Val Ser Thr Lys
199          465                      470                      475                      480
200      Pro Thr Arg Thr Ser Lys Val Arg Gln Leu Leu Asp Thr Thr Asp Ile
201          485                      490                      495
202      Gln Gly Glu Glu Phe Ala Lys Val Ile Val Gln Lys Leu Lys Asp Asn
203          500                      505                      510
204      Lys Gln Met Gly Leu Gln Pro Tyr Pro Glu Ile Leu Val Val Ser Arg
205          515                      520                      525
206      Ser Pro Ser Leu Asn Leu Leu Gln Asn Lys Ser Met
207          530                      535                      540
209 <210> SEQ ID NO: 3
210 <211> LENGTH: 1620
211 <212> TYPE: DNA
212 <213> ORGANISM: Homo sapiens
213 <400> SEQUENCE: 3
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216      cgcgctccagg tggccgtgaa gcacctgcac atccacactc cgctgctcga cagtgaagaa      180
217      aaggatgtct taagagaagc tgaaatttta cacaagcta gatttagtta cattctcca      240
218      attttgggaa tttgcaatga gctgaattt ttgggaatag ttactgaata catgccaaat      300
219      ggatcattaa atgaactcct acataggaaa actgaatata ctgatgttgc ttggccattg      360
220      agatttcgca tcctgcatga aattgccctt ggtgtaaatt acctgcacaa tatgactcct      420
221      cctttacttc atcatgactt gaagactcag aatatcttat tggacaatga atttcattgt      480
222      aagattgcag attttggtt atcaaagtgg cgcattgatg cctctcaca gtcacgaagt      540
223      agcaaactctg caccagaagg agggacaatt atctatatgc cacctgaaaa ctatgaacct      600
224      ggacaaaaat caagggccag tatcaagcac gatatatata gctatgcagt tatcacatgg      660
225      gaagtgttat ccagaaaaca gccttttgaa gatgtcacca atcctttgca gataatgtat      720
226      agtgtgtcac aaggacatcg acctgttatt aatgaagaaa gtttgccata tgatatacct      780
227      caccgagcac gtatgatctc tctaatagaa agtggatggg cacaaaatcc agatgaaaga      840
228      ccatctttct taaaatgttt aatagaactt gaaccagttt tgagaacatt tgaagagata      900
229      acttttcttg aagctgttat tcagctaaag aaaacaaagt tacagagtgt ttcaagtgcc      960
230      attcacctat gtgacaagaa gaaaatggaa ttatctctga acatacctgt aaatcatggt      1020
231      ccacaagagg aatcatgtgg atcctctcag ctccatgaaa atagtggttc tcctgaaact      1080
232      tcaaggtccc tgccagctcc tcaagacaat gattttttat ctagaaaagc tcaagactgt      1140
233      tattttatga agctgcatca ctgtcctgga aatcacagtt gggatagcac cattttctgga      1200
234      tctcaaaggg ctgcattctg tgatcacaa accattccat gctcttcagc aataataaat      1260
235      ccaactctcaa ctgcaggaaa ctcagaacgt ctgcagcctg gtatagccca gcagtggatc      1320
236      cagagcaaaa gggaagacat tgtgaaccaa atgacagaag cctgccttaa ccagtgccta      1380
237      gatgcccttc tgtccaggga cttgatcatg aaagaggact atgaacttgt tagtaccaag      1440
238      cctacaagga cctcaaaagt cagacaatta ctagacacta ctgacatcca aggagaagaa      1500
239      tttgccaaag ttatagtaca aaaattgaaa gataacaaac aaatgggtct tcagccttac      1560
240      ccggaaatac ttgtggtttc tagatcacca tctttaaatt tacttcaaaa taaaagcatg      1620
242 <210> SEQ ID NO: 4
243 <211> LENGTH: 300
244 <212> TYPE: PRT
245 <213> ORGANISM: Homo sapiens
246 <400> SEQUENCE: 4

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